```
?ds

Set     Items   Description
S1      25734   MOYER? OR PARKS?
S2         27   S1 AND CULTIVAR
S3          0   S2 AND NUCLEIC
S4         27   S2
S5         20   RD (unique items)
S6        454   S1 AND (DNA OR NUCLEOTIDE OR NUCLEIC OR POLYNUCLEOTIDE)
S7        172   S6 AND (SNP OR POLYMORPH? OR MUTANT OR FINGERPRINT?)
S8        132   RD (unique items)
S9        115   S8 AND (IDENTIF? OR DETECT? OR AMPLIF? OR SEPARATE OR SCRE-
              EN OR ISOLATE)
S10        52   S9 AND PLANT
S11         0   S10 AND (CULTIVAR OR SPECIE)
S12        18   S10 AND (AFLP OR RFLP OR RAPD OR SSR)
S13         1   S10 AND DAF
S14   1790624   (SNP OR POLYMORPH? OR MUTANT OR FINGERPRINT?)
S15    586890   S14 AND (IDENTIF? OR DETECT? OR AMPLIF? OR SEPARATE OR SCR-
              EEN OR SEPARATE)
S16      5707   S15 AND CULTIVAR
S17      3581   S16 AND (AFLP OR RAPD OR RFLP OR SSR OR DAF)
S18        11   S17 AND POINSETTIA
S19         5   RD (unique items)
S20     48151   S14 AND (FINGERPRINT OR PROFILE)
S21      1681   S20 AND DATABASE
S22       898   S21 AND (COMPAR? OR CLUSTER OR GROUP OR CLASSIF?)
S23       165   S22 AND (UNKNOWN OR UNIDENTIFIED OR DISTINGUISH)
S24         1   S23 AND INDEX(W3)VALUE
S25       101   S23 AND (DICE OR (SIMILAR?)(W3)(COEFFICIEN?) OR SIMILAR? OR
               DISSIMILAR?)
S26       313   S22 AND (DICE OR (SIMILAR?)(W3)(COEFFICIEN?) OR SIMILAR? OR
               DISSIMILAR?)
S27       101   S25
S28        87   RD (unique items)
S29         8   S28 AND ZERO
S30        92   S26 AND (INDEX OR VALUE OR ZERO)
S31        85   RD (unique items)
S32        46   S31 AND PY<=2000
S33       149   S26 AND PY<=2000 NOT S46
S34         7   S33 AND GENOTYPE AND PHENOTYPE
S35       109   S26 NOT PY>2000 NOT S32
S36        68   RD (unique items)
S37         4   S36 AND GENOTYPE AND PHENOTYPE
S38         7   S36 AND GENOTYPE
S39         3   S38 NOT S37
S40         1   S38 AND (LYNCH OR DICE)
S41         0   S36 AND (LYNCH OR DICE OR JACCARD)(W)(MODEL OR METHOD)
S42         0   S36 AND (LYNCH OR DICE OR JACCARD)(W5)(MODEL OR METHOD)
S43       546   (LYNCH OR DICE OR JACCARD) AND (SIMILAR? OR DISSIMILAR?) A-
              ND (SNP OR POLYMORPHISM)
S44        17   S43 AND DATABASE
S45        16   RD (unique items)
?
```

DIALOG (BIOTECH)
1/16/04

TD001 TEMP

Nucleic acid scanning techniques distinguish closely related cultivars of poinsettia
AUTHOR: Starman Terri Woods (Reprint); Duan Xiangrong (Reprint); Abbitt Shane (Reprint)
AUTHOR ADDRESS: Department of Ornamental Horticulture and Landscape Design, Institute of Agriculture, University of Tennessee, Knoxville, TN, 37901-1071, USA**USA
JOURNAL: Hortscience 34 (6): p1119-1122 Oct., 1999 1999
MEDIUM: print
ISSN: 0018-5345
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: DNA **amplification fingerprinting** (**DAF**) was used to evaluate the genetic relationships among 11 cultivars of **poinsettia** (Euphorbia pulcherrima Willd.). **Amplification** was with 10 octamer oligonucleotide primers that generated 336 DNA bands. Thirty-one percent of the bands were **polymorphic** and distinguished among cultivars. Genetic relationships were evaluated by cluster analysis, and the resulting dendrogram closely agreed with published **cultivar** relationships. Arbitrary signatures from **amplification** profiles (ASAP) were further used to characterize two cultivars, 'Nutcracker Red' and 'Peterstar Red', that were previously found to be genetically and morphologically similar, as well as five cultivars in the "Freedom" series. The **DAF** products generated with arbitrary octamer primers were reamplified with mini-hairpin decamer primers in these experiments. The ASAP profiles were complex and yielded a total of 231 bands, 38% of which were **polymorphic** and capable of distinguishing each Freedom **cultivar** . Five of the eight primer combinations distinguished 'Nutcracker Red' from 'Peterstar Red'. Thus, closely related cultivars of **poinsettia** can be separated using new and improved molecular **fingerprinting** protocols.

18/3,AB/2 (Item 2 from file: 5)
DIALOG(R)File 5:Biosis Previews(R)

0010869409 BIOSIS NO.: 199799503469
Identification **of** poinsettia **cultivars using** RAPD **markers**
AUTHOR: Ling Jing-Tian; Sauve Roger; Gawel Nick
AUTHOR ADDRESS: Cooperative Agric. Res. Program, Tenn. State Univ., Nashville, TN 37209-1561, USA**USA
JOURNAL: Hortscience 32 (1): p122-124 1997 1997
ISSN: 0018-5345
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Randomly **amplified polymorphic** DNA (**RAPD**) techniques were used to compare the DNA from leaf tissues of nine commercial **poinsettia** (Euphorbia pulcherrima Wild ex Klotzsch) cultivars. **Amplification** occurred in 57 out of 60 (95%) tested primers. Nine primers that revealed **polymorphisms** among cultivars were selected for further evaluation. Forty-eight **RAPD** bands were scored from these primers, and 33 (69%) were **polymorphic** . All tested cultivars could be discriminated with seven bands generated from primers OPB7 and OPC13. Results of a UPGMA cluster analysis and principal components analysis placed the nine cultivars into two groups: one group consisted of 'Jingle Bells', 'Supjibil', and 'V-17 Angelika', the other of 'V-14 Glory', 'Red Sails', 'Jolly Red', and 'Freedom'. 'Lilo Red' and 'Pink Peppermint' belonged to the latter group, but were relatively distant from other cultivars in that group. These results indicate that RAPDs are efficient for **identification** of **poinsettia** cultivars and for determination of the genetic relationships among cultivars.

18/3,AB/3 (Item 1 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

08088949 Genuine Article#: 245XK Number of References: 15
Title: Nucleic acid scanning techniques distinguish closely related cultivars of poinsettia (ABSTRACT AVAILABLE)
Author(s): Starman TW (REPRINT) ; Duan XR; Abbitt S
Corporate Source: UNIV TENNESSEE,INST AGR, DEPT ORNAMENTAL HORT & LANDSCAPE DESIGN/KNOXVILLE//TN/37901 (REPRINT)
Journal: HORTSCIENCE, 1999, V34, N6 (OCT), P1119-1122
ISSN: 0018-5345 Publication date: 19991000
Publisher: AMER SOC HORTICULTURAL SCIENCE, 701 NORTH SAINT ASAPH STREET, ALEXANDRIA, VA 22314-1998
Language: English Document Type: ARTICLE
Abstract: DNA **amplification fingerprinting** (**DAF**) was used to evaluate the genetic relationships among 11 cultivars of **poinsettia** (Euphorbia pulcherrima Willd.). **Amplification** was with 10 octamer oligonucleotide primers that generated 336 DNA bands. Thirty-one percent of the bands were **polymorphic** and distinguished among cultivars. Genetic relationships were evaluated by cluster analysis, and the resulting dendrogram closely agreed with published **cultivar** relationships. Arbitrary signatures from **amplification** profiles (ASAP) were further used to characterize two cultivars, 'Nutcracker Red' and 'Peterstar Red', that were previously found to be genetically and morphologically similar, as well as five cultivars in the ''Freedom'' series. The **DAF** products generated with arbitrary octamer primers were reamplified with mini-hairpin decamer primers in these experiments. The ASAP profiles were complex and yielded a total of 231 bands, 38% of which were **polymorphic** and capable of distinguishing each Freedom **cultivar** . Five of the eight primer combinations distinguished 'Nutcracker Red' from 'Peterstar Red'. Thus, closely related cultivars of **poinsettia** can be separated using new and improved molecular **fingerprinting** protocols.

18/3,AB/4 (Item 1 from file: 71)
DIALOG(R)File 71:ELSEVIER BIOBASE

01258657 1999239722
Nucleic acid scanning techniques distinguish closely related cultivars of poinsettia
Woods Starman T.; Duan X.; Abbitt S.
ADDRESS: T. Woods Starman, Dept. of Ornamental Horticulture, Institute of Agriculture, University of Tennessee, Knoxville, TN 37901-1071, United States
Journal: HortScience, 34/6 (1119-1122), 1999, United States
CODEN: HJHSA
ISSN: 0018-5345
DOCUMENT TYPE: Conference Paper
LANGUAGES: English SUMMARY LANGUAGES: English
NO. OF REFERENCES: 15

DNA **amplification fingerprinting** (**DAF**) was used to evaluate the genetic relationships among 11 cultivars of **poinsettia** (Euphorbiapulcherrima Willd). **Amplification** was with 10 octamer oligonucleotide primers that generated 336 DNA bands. Thirty-one percent of the bands were **polymorphic** and distinguished among cultivars. Genetic relationships were evaluated by cluster analysis, and the resulting dendrogram closely agreed with published **cultivar** relationships. Arbitrary signatures from **amplification** profiles (ASAP) were further used to characterize two cultivars, 'Nutcracker Red' and 'Peterstar Red', that were previously found to be genetically and morphologically similar, as well as five cultivars in the 'Freedom' series. The **DAF** products generated with arbitrary octamer primers were reamplified with mini-hairpin decamer primers in these experiments. The ASAP profiles were complex and yielded a total of 231 bands, 38 % of which were **polymorphic** and capable of distinguishing each Freedom **cultivar** . Five of the eight primer combinations distinguished 'Nutcracker Red' from 'Peterstar Red'. Thus, closely related cultivars of **poinsettia** can be separated using new and

improved molecular **fingerprinting** protocols.

18/3,AB/5 (Item 1 from file: 144)
DIALOG(R)File 144:Pascal

14331884 PASCAL No.: 99-0540359
Nucleic acid scanning techniques distinguish closely related cultivars of poinsettia
STARMAN T W; XIANGRONG DUAN; ABBITT S
Department of Ornamental Horticulture and Landscape Design, Institute of Agriculture, University of Tennessee, Knoxville, TN 37901-1071, United States
Journal: HortScience, 1999, 34 (6) 1119-1122
Language: English
DNA **amplification** **fingerprinting** (**DAF**) was used to evaluate the genetic relationships among 11 cultivars of **poinsettia** (Euphorbia pulcherrima Willd.). **Amplification** was with 10 octamer oligonucleotide primers that generated 336 DNA bands. Thirty-one percent of the bands were **polymorphic** and distinguished among cultivars. Genetic relationships were evaluated by cluster analysis, and the resulting dendrogram closely agreed with published **cultivar** relationships. Arbitrary signatures from **amplification** profiles (ASAP) were further used to characterize two cultivars, 'Nutcracker Red' and 'Peterstar Red', that were previously found to be genetically and morphologically similar, as well as five cultivars in the "Freedom" series. The **DAF** products generated with arbitrary octamer primers were reamplified with mini-hairpin decamer primers in these experiments. The ASAP profiles were complex and yielded a total of 231 bands, 38% of which were **polymorphic** and capable of distinguishing each Freedom **cultivar** . Five of the eight primer combinations distinguished 'Nutcracker Red' from 'Peterstar Red'. Thus, closely related cultivars of **poinsettia** can be separated using new and improved molecular **fingerprinting** protocols.

RPT

Development and characterization of polymorphic **microsatellites from Prunus avium 'Napoleon'.**

AUTHOR: Clarke J B (Reprint); Tobutt K R
AUTHOR ADDRESS: Horticulture Research International, East Malling, West Malling, Kent, ME19 6BJ, UK**UK
AUTHOR E-MAIL ADDRESS: jacob.clarke@hri.ac.uk
JOURNAL: Molecular Ecology Notes 3 (4): p578-580 December 2003 2003
MEDIUM: print
ISSN: 1471-8278 _(ISSN print)
DOCUMENT TYPE: Article
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Primers were developed for 21 microsatellite loci isolated by enrichment from Prunus avium 'Napoleon'. Twelve loci contained uninterrupted dinucleotide repeats and nine were more complex. Nineteen primer pairs (EMPA001-019) showed single locus **polymorphisms** in a **cultivar** survey of 14 sweet cherries, with two to seven alleles per locus. Three primer pairs in combination (EMPA014, 015 and 018) discriminated all cultivars. Two primer pairs for loci monomorphic in P. avium were included: EMPA020 revealed segregation in an interspecific progeny and EMPA021 revealed **polymorphism** in P. dulcis. Twelve primer pairs reliably **amplified** products in three peach cultivars of which seven revealed **polymorphisms** .

Ordered

March 1, 71

A database **system for fragment patterns of genomic DNA of Staphylococcus aureus**

CLAUS H; CUNY C; PASEMANN B; WITTE W

Robert Koch-Institut, Bereich Wernigerode, Burgstrasse 37, 38855 Wernigerode, Germany

National Workshop on Catheter-related Infections, 2 (Cologne DEU) 1995-11-23

Journal: Zentralblatt fuer Bakteriologie, 1998, 287 (1-2) 105-116

Language: English

The increasing use of molecular **fingerprints** in the epidemiology of bacterial nosocomial infections urgently demands a computerised analysis and storage of corresponding patterns, especially with regard to results obtained at different times and in different laboratories. This paper presents a **database** system in connection with **cluster** analysis of clonal relations by using genomic DNA fragment patterns of S. aureus (SmaI-digestion, pulsed-field gel electrophoresis) as an example: The **database** is operated under MS-Access, version 2.0. The **cluster** analysis is based on an optimising **similarity** algorithm.

Title: Unsupervised data base clustering based on daylight's fingerprint **and Tanimoto** similarity **: A fast and automated way to** cluster **small and large data sets**

Author: Butina, Darko

Corporate Source: Glaxo Wellcome Research and Development, Hertfordshire, UK

Source: Journal of Chemical Information and Computer Sciences v 39 n 4 1999. p 747-750

Publication Year: 1999

CODEN: JCISD8 ISSN: 0095-2338

Language: English

Abstract: One of the most commonly used clustering algorithms within the worldwide pharmaceutical industry is Jarvis-Patrick's (J-P). The implementation of J-P under Daylight software, using Daylight's **fingerprints** and the Tanimoto **similarity index** , can deal with sets of 100 k molecules in a matter of a few hours. However, the J-P clustering algorithm has several associated problems which make it difficult to **cluster** large data sets in a consistent and timely manner. The clusters produced are greatly dependent on the choice of the two parameters needed to run J-P clustering, such that this method tends to produce clusters which are either very large and heterogeneous or homogeneous but too small. In any case, J-P always requires time-consuming manual tuning. This paper describes an algorithm which will identify dense clusters where **similarity** within each **cluster** reflects the Tanimoto **value** used for the clustering, and, more importantly, where the **cluster** centroid will be at least **similar** , at the given Tanimoto **value** , to every other molecule within the **cluster** in a consistent and automated manner. The **similarity** term used throughout this paper reflects the overall **similarity** between two given molecules, as defined by Daylight's **fingerprints** and the Tanimoto **similarity index** . (Author abstract) 7 Refs.

32/3,AB/2 (Item 2 from file: 8)

DIALOG(R)File 8:Ei Compendex(R)

04384103

E.I. No: EIP96043141128

Title: Fingerprint classification

Author: Karu, Kalle; Jain, Anil K.

Corporate Source: Michigan State Univ, East Lansing, MI, USA

Source: Pattern Recognition v 29 n 3 Mar 1996. p 389-404

Publication Year: 1996

CODEN: PTNRA8 ISSN: 0031-3203

Language: English

Abstract: A **fingerprint classification** algorithm is presented in this paper. **Fingerprints** are **classified** into five categories: arch, tented arch, left loop, right loop and whorl. The algorithm extracts singular points (cores and deltas) in a **fingerprint** image and performs **classification** based on the number and locations of the detected singular points. The **classifier** is invariant to rotation, translation and small amounts of scale changes. The **classifier** is rule-based, where the rules are generated independent of a given data set. The **classifier** was tested on 4000 images in the NIST-4 **database** and on 5400 images in the NIST-9 **database** . For he NIST-4 **database** , **classification** accuracies of 85.4% for the five-class problem and 91.1% for the four-class problem (with arch and tented arch placed in the same category) were achieved. Using a reject option, the four-class **classification** error can be reduced to less than 6% with 10% **fingerprint** images rejected. **Similar classification** performance was obtained on the NIST-9 **database** . (Author abstract) 14 Refs.

32/3,AB/3 (Item 1 from file: 34)

DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

09350933 Genuine Article#: 394ZG Number of References: 38

Title: Toxicogenomics-based discrimination of toxic mechanism in HepG2

human hepatoma cells (ABSTRACT AVAILABLE)
Author(s): Burczynski ME; McMillian M; Ciervo J; Li L; Parker JB; Dunn RT; Hicken S; Farr S; Johnson MD (REPRINT)
Corporate Source: Robert Wood Johnson Pharmaceut Res Inst,Drug Safety Evaluat,POB 300,Route 202/Raritan//NJ/08869 (REPRINT); Robert Wood Johnson Pharmaceut Res Inst,Drug Safety Evaluat,Raritan//NJ/08869; Phase 1 Mol Toxicol Inc,Santa Fe//NM/87505
Journal: TOXICOLOGICAL SCIENCES, **2000** , V58, N2 (DEC), P399-415
ISSN: 1096-6080 Publication date: 20001200
Publisher: OXFORD UNIV PRESS, GREAT CLARENDON ST, OXFORD OX2 6DP, ENGLAND
Language: English Document Type: ARTICLE
Abstract: The rapid discovery of sequence information from the Human Genome Project has exponentially increased the amount of data that can be retrieved from biomedical experiments. Gene expression profiling, through the use of microarray technology, is rapidly contributing to an improved understanding of global, coordinated cellular events in a variety of paradigms. In the field of toxicology, the potential application of toxicogenomics to indicate the toxicity of unknown compounds has been suggested but remains largely unsubstantiated to date. A major supposition of toxicogenomics is that global changes in the expression of individual mRNAs (i.e., the transcriptional responses of cells to toxicants) will be sufficiently distinct, robust, and reproducible to allow discrimination of toxicants from different classes. Definitive demonstration is still lacking for such specific "genetic **fingerprints** ," as opposed to nonspecific general stress responses that may be indistinguishable between compounds and therefore not suitable as probes of toxic mechanisms. The present studies demonstrate a general application of toxicogenomics that distinguishes two mechanistically unrelated classes of toxicants (cytotoxic anti-inflammatory drugs and DNA-damaging agents) based solely upon a **cluster** -type analysis of genes differentially induced or repressed in cultured cells during exposure to these compounds. Initial **comparisons** of the expression patterns for 100 toxic compounds, using all **similar** to 250 genes on a DNA microarray(**similar** to 2.5 million data points), failed to discriminate between toxicant classes. A major obstacle encountered in these studies was the lack of reproducible gene responses, presumably due to biological variability and technological limitations. Thus multiple replicate observations for the prototypical DNA damaging agent, cisplatin, and the non-steroidal anti-inflammatory drugs (NSAIDs) diflunisal and flufenamic acid were made, and a subset of genes yielding reproducible inductions/repressions was selected for **comparison** . Many of the " **fingerprint** genes" identified in these studies were consistent with previous observations reported in the literature (e.g., the well-characterized induction by cisplatin of p53-regulated transcripts such as p21(waf1/cip1) and PCNA [proliferating cell nuclear antigen]). These gene subsets not only discriminated among the three compounds in the learning set but also showed predictive **value** for the rest of the **database** (**similar** to 100 compounds of various toxic mechanisms). Further refinement of the clustering strategy, using a computer-based optimization algorithm, yielded even better results and demonstrated that genes that ultimately best discriminated between DNA damage and NSAIDs were involved in such diverse processes as DNA repair, xenobiotic metabolism, transcriptional activation, structural maintenance, cell cycle control, signal transduction, and apoptosis. The determination of genes whose responses appropriately **group** and dissociate anti-inflammatory versus DNA-damaging agents provides an initial paradigm upon which to build for future, higher throughput-based identification of toxic compounds using gene expression patterns alone.

32/3,AB/4 (Item 2 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

08697420 Genuine Article#: 318VB Number of References: 25
Title: Comparing **DNA** fingerprints **of infectious organisms** (ABSTRACT AVAILABLE)
Author(s): Segal MR (REPRINT) ; Salamon H; Small PM

Corporate Source: UNIV CALIF SAN FRANCISCO,DEPT EPIDEMIOL & BIOSTAT/SAN FRANCISCO//CA/94143 (REPRINT); BERLEX LABS INC,/RICHMOND//CA/94804; STANFORD UNIV,MED CTR, DIV INFECT DIS & GEOG MED/STANFORD//CA/94305
Journal: STATISTICAL SCIENCE, **2000** , V15, N1 (FEB), P27-45
ISSN: 0883-4237 Publication date: 20000200
Publisher: INST MATHEMATICAL STATISTICS, IMS BUSINESS OFFICE-SUITE 7, 3401 INVESTMENT BLVD, HAYWARD, CA 94545
Language: English Document Type: ARTICLE
Abstract: Genotypes of infectious organisms are becoming the foundation for epidemiologic studies of infectious disease. Central to the use of such data is a means for **comparing** genotypes. We develop methods for this purpose in the context of DNA **fingerprint** genotyping of tuberculosis, but our approach is applicable to many **fingerprint** -based genotyping systems and/or organisms. Data available on replicate (laboratory) strains here reveal that (i) error in **fingerprint** band size is proportional to band size and (ii) errors are positively correlated within a **fingerprint** . **Comparison** (or matching) scores computed to account for this error structure need to be ''standardized'' in order to properly rank the **comparisons** . We demonstrate the utility of using extreme **value** distributions to effect such standardization. Several estimation issues for the extreme **value** parameters are discussed, including a lack of robustness of (approximate) maximum likelihood estimates. Interesting findings to emerge from examination of quantiles of standardized matching scores include (i) formal significance is not attainable when querying a **database** for a given **fingerprint** pattern and (ii) maximal matching probabilities are not necessarily monotonely decreasing with increasing numbers of **fingerprint** bands.

32/3,AB/5 (Item 3 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci

03549471 Genuine Article#: PM113 Number of References: 43
Title: SEQUENCE DIVERGENCE ANALYSIS FOR THE PREDICTION OF 7-HELIX MEMBRANE-PROTEIN STRUCTURES .1. COMPARISON **WITH BACTERIORHODOPSIN** (Abstract Available)
Author(s): DU P; ALKORTA I
Corporate Source: SYNAPT PHARMACEUT CORP,215 COLL RD/PARAMUS//NJ/07652; MOLEC RES INST/PALO ALTO//CA/94304
Journal: PROTEIN ENGINEERING, **1994** , V7, N10 (OCT), P1221-1229
ISSN: 0269-2139
Language: ENGLISH Document Type: ARTICLE
Abstract: A method using protein sequence divergence to predict the three-dimensional structure of the transmembrane domain of seven-helix membrane proteins is described. The key component in the multistep procedure is the calculation of a hydrophilic and lipophilic variability **index** for each amino acid in an alignment of a family of homologous proteins. The variability **profile** , a plot of the calculated variability **index** versus alignment position, can be used to predict a tertiary model of the backbone conformation of the transmembrane domain. This method was applied to bacteriorhodopsin (BR) and the model obtained was **compared** with the known structure of this protein. Using an alignment of the amino acid sequences of BR and closely related (greater than or equal to 20% identity) proteins, the boundaries of the transmembrane regions, their secondary structures and orientations inside the membrane bilayer were predicted based on the variability **profile** . Additional information about the shape of the helix bundle was also obtained from the average variability of each transmembrane helix with the assumption that the helices are packed sequentially and form a closed helix bundle. Correct features of the known structure of BR were found in the model structure, suggesting that a **similar** strategy can be used to predict transmembrane helices and the packing shape of other membrane proteins with seven transmembrane helices, such as the opsins and other G-protein coupled receptors.

Genotypic diversity among Aeromonas isolates recovered from drinking water production plants as revealed by AFLP SUP T SUP M analysis

HUYS G; KERSTERS I; COOPMAN R; JANSSEN P; KERSTERS K

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Journal: Systematic and applied microbiology, **1996** , 19 (3) 428-435

Language: English

A novel DNA **fingerprinting** method, named AFLP, was used to determine the genotypic diversity among 168 Aeromonas isolates originating from five drinking water production plants in Flanders, Belgium. The AFLP technique determines the genomic **similarity** between bacterial strains through numerical analysis of banding patterns generated by the electrophoretic separation of selectively amplified restriction fragments. Using an identification library (AERO94) comprising AFLP **fingerprints** of 107 well-characterized Aeromonas strains, a total of 144 isolates (86%) could be allocated to one of the 14 DNA hybridization groups (HGs) so far recognized in the genus Aeromonas. The majority of these strains belonged to Aeromonas hydrophila HGs 2 and 3, Aeromonas caviae HGs 5A and 5B SUB 1 Aeromonas sobria HG 7, and Aeromonas veronii HG8/10. **Cluster** analysis of individual banding patterns revealed that eight isolates identified as Aeromonas eucrenophila HG6 were dispersed over two well-separated AFLP clusters, suggesting the existence of a genotypic subdivision within this species. The remaining 24 unidentified isolates constituted a homogeneous AFLP **cluster** which was found to be most closely related to HG2. Possibly, these strains may represent a currently unknown HG within the A. hydrophila complex. In conclusion, this study clearly elucidates the taxonomic **value** of the AERO94 **database** for the identification and **classification** of unknown aeromonads and further demonstrates the general applicability of AFLP-based libraries to determine genotypic relationships in other bacterial genera.

ordered

First searchable database **for DNA profiles of human cell lines: sequential use of** fingerprint **techniques for authentication.**

Dirks W; MacLeod R A; Jager K; Milch H; Drexler H G

DSMZ-German Collection of Microorganisms and Cell Cultures, Department of Human and Animal Cell Lines, Braunschweig, Germany. wdi@dsmz.de

Cellular and molecular biology (Noisy-le-Grand, France) (FRANCE) Sep **1999** , 45 (6) p841-53, ISSN 0145-5680 Journal Code: 9216789

Document type: Journal Article

Languages: ENGLISH

Main Citation Owner: NLM

Record type: Completed

The authenticity and freedom from cross-contaminants of a cell line are important prerequisites for any research, development or production programs involving cell lines. Mini- and microsatellites in the human genome harboring variable-numbers of tandem repeat (VNTR) DNA markers allow individualization at the DNA level and are of practical **value** for genetic linkage mapping, forensic legal medicine, paternity testing, monitoring of bone marrow transplants, and individualization of established cell lines. We have validated **fingerprint** techniques of different single- and multiple-locus VNTRs enabling the establishment of a searchable **database** of DNA profiles. As a result, multiplexed polymerase chain reaction amplification fragment length **polymorphism** (AmpFLP) of four prominent and highly **polymorphic** minisatellite VNTR loci was proven as the best tool for screening the uniqueness of DNA profiles in a **fingerprint database** . In order to avoid false positivity, identical or **similar** DNA profiles based on AmpFLP VNTR were tested further using a multi-locus **fingerprint** system. Our data demonstrate that misidentification remains a chronic problem among human continuous cell lines (detailed information at URL http://www.dsmz.de). The combination of rapidly generated DNA profiles based on single-locus VNTR loci, their authentication by screening the **fingerprint database** , and confirmation of duplicate banding patterns using multilocus **fingerprints** constitute a highly reliable and robust method, which enables high fidelity and quality of maintenance independent from the quantity of individual cell lines.

Genetic relationships among and within Shigella flexneri serotypes based on Fluorescence Amplified Fragment Length Polymorphism **fingerprinting.**

AUTHOR: Sirisriro A (Reprint); Sethabutr O (Reprint); Mason C (Reprint); Venkatesan M
AUTHOR ADDRESS: USAMC-AFRIMS, Bangkok, Thailand**Thailand

JOURNAL: Abstracts of the General Meeting of the American Society for Microbiology 103 pC-398 2003 2003
MEDIUM: cd-rom
CONFERENCE/MEETING: 103rd American Society for Microbiology General Meeting Washington, DC, USA May 18-22, 2003; 20030518
SPONSOR: American Society for Microbiology
ISSN: 1060-2011 _(ISSN print)
DOCUMENT TYPE: Meeting; Meeting Abstract
RECORD TYPE: Abstract
LANGUAGE: English

ABSTRACT: Background: Shigella flexneri becomes predominated etiologic agent of bacillary dysentery and causes public health problems worldwide. Although S. flexneri is assigned into various serotypes based on antigenic properties, genotypic relationship among different serotypes has not yet been demonstrated. In this study, we used Florescence Amplified Fragment Length **Polymorphism** (AFLP), which is based on selective amplification of restriction fragments of genomic DNA, to reveal the genetic relatedness within and between a variety of S. flexneri serotypes. Methods: Fluorescence AFLP was performed on a collection of clinical S. flexneri isolates from Kenya, Bangladesh, Nepal, Vietnam and Thailand (n=112). The experiment involved digestion of bacterial genomic DNA by a pair of restriction enzyme, MseI and EcoRI, followed by ligation with complementary adaptors and preselective amplification. A subset of preselective amplification product was selectively amplified by three modules of fluorescence primers. The selective amplification products were subsequently separated by gel electrophoresis through an automated sequencer. **Similarity** was calculated by band-based **Dice** coefficient and cluster analysis were performed by using UPGMA. Results: The AFLP pattern of individual isolates yielded an average of 109 bands, ranging between 60-500 bp derived from three primer sets: EcoRI-A/MseI-C, EcoRI-G/MseI-C, and EcoRI-G/MseI-A. Banding profiles of S. flexneri based on serotypes 1, 2a, 3a, 4 and 6 were clearly distinguished. **Similarity** analysis demonstrated the **similarity** between individual profiles ranging from 78-98% within each serotypes. It was observed that the genetic relationships among serotypes 1, 2a, 3 and 4 were closely related while the serotype 6 was separately clustered. Conclusion: Standard AFLP using three selective primer sets of EcoRI and MseI allows a sufficient discrimination between different serotypes and strains of S. flexneri. The unique banding profiles of each serotype can be applied as a **database** for categorizing untypable strains.

Characterization of a subcloned fragment (pBA0.6) of pCMM86 located on 17q21 and its potential use in generating an individual-specific DNA profile

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Sequence analysis was carried out of a truman clone pBA0.6 generated after exonuclease III/S1 nuclease digestion and subcloning of pCMM86 (GDB: 168382, D17S74), which was not available in the **database** . It revealed the presence of a reiterating core motif of 24mer GTGGGTGTGTTGGAGGGGGTGAGG, present 23 times, which was GC-rich and minisatellitic in nature. Genomic blots of HaeIII-digested human DNA, when hybridized with pBA0.6, generated a ladder of bands between 29.0 kb and 2.1 kb. Hybridization analyses of 88 unrelated individuals belonging to four regions of India using this probe revealed polymorphic bands which were individual specific. The probability of identity ranged from 5.07 x 10sup -sup 1sup 4 in Punjabis to 2.64 x 10sup -sup 1sup 6 in Bengalis and was found to be 3.06 x 10sup -sup 1sup 6 in UPites, whereas in the case of South Indians, it was 3.9 x 10sup -sup 1sup 5. Three sets of isomorphic bands at 29.0 kb, 2.4 kb, and 2.1 kb were common between the individuals of all the regions and served as internal markers. The 29.0-kb band was observed to be Homo sapiens specific. Construction of dendrograms based on the UPGMA method with **Jaccard** 's coefficient values suggested less genetic **similarity** /high genetic diversity in all the population groups, indicating that the samples taken were random. Maximum likelihood estimates through the bootstrap sampling method showed that Punjabis, Bengalis, anti UPites formed one cluster, whereas South Indians formed a separate cluster, altogether thus showing the proximity of these three population groups compared with that from South India. A preliminary study by Northern hybridization with pBA0.6 resulted in two transcripts of 0.63 kb and 0.29 kb. This finding was corroborated with RT-PCR results where 2 amplicons, matching the expected size of two open reading frames within the minisatellite sequence, were obtained. The role of the two transcripts from the minisatellite sequence is not clear as yet, and it is probable that these messages may not get translated because of the absence of a eukaryotic Kozak sequence around the initiator methionine in the pBA0.6 sequence.

RAPDs and noncoding chloroplast DNA reveal a single origin of the cultivated Allium fistulosum from A. altaicum (Alliaceae).

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ABSTRACT: The origin of the crop species Allium fistulosum (bunching onion) and its relation to its wild relative A. altaicum were surveyed with a restriction fragment length **polymorphism** (RFLP) analysis of five noncoding cpDNA regions and with a random amplified polymorhic DNA (RAPD) analysis of nuclear DNA. Sixteen accessions of A. altaicum, 14 accessions of A. fistulosum, representing the morphological variability of the species, and five additional outgroup species from Allium section Cepa were included in this study. The RFLP analysis detected 14 phylogenetically informative character transformations, whereas RAPD revealed 126 polymorphic fragments. Generalized parsimony, neighbor-joining analysis of genetic distances, and a principal co-ordinate analysis were able to distinguish the two species, but only RAPD data allowed clarification of the interrelationship of the two taxa. The main results of this investigation were: (1) A. fistulosum is of monophyletic origin, and (2) A. fistulosum originated from an A. altaicum progenitor, making A. altaicum a paraphyletic species. Compared with A. altaicum the cultivated accessions of the bunching onion show less genetic variability, a phenomenon that often occurs in crop species due to the severe genetic bottleneck of domestication. Allium altaicum and A. fistulosum easily hybridize when grown together, and most garden-grown material is of recent hybrid origin.

ordered

Differentiation of bermudagrass (Cynodon spp.) genotypes by AFLP analyses
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ABSTRACT: Bermudagrasses (Cynodon spp.) are major turfgrasses for home lawns, public **parks** , golf courses and sport fields, and are widely adapted to tropical and warmer temperate climates. Morphological and physiological characteristics are not sufficient to differentiate some bermudagrass genotypes because the differences between them are often subtle and subject to environmental influence. In this study, a **DNA** -typing technique, **amplified** fragment length **polymorphism** (**AFLP**), was used to differentiate bermudagrass genotypes and to explore their genetic relationships. Twenty seven bermudagrass cultivars and introductions, mostly from the Coastal Plain Experiment Station in Tifton, Ga., were assayed by the radioactive (32P) and the fluorescence-labeled **AFLP** methods. The **AFLP** technique produced enough **polymorphism** to differentiate all 27 bermudagrass genotypes, even the closely related ones. An average of 48-74 bands in the 30-600-bp size range was **detected** by the 32P-labeled **AFLP** method. Theresults indicated that most of the 14 primer combinations tested in this study could be used to distinguish bermudagrass genotypes, and that some single primer-pairs could differentiate all 27 of them. To test the reliability and reproducibility of the **AFLP** procedure, three **DNA** isolations (replications) of the 27 bermudagrass genotypes were assayed using five primer pairs. Only 0.6% of the bands were evaluated differently among the three replications. One replication of one genotype (which was most likely a planting contaminant) was grouped in an unexpected cluster using the Unweighted Pair Group Mean Average (UPGMA) method. A one- or two-band difference in scoring did not change the clustering of genotypes or the replications within genotypes. The 27 genotypes were grouped into three major clusters, many of which were in agreement with known pedigrees. Trees constructed with different primer combinations using 32P-and fluorescence-labelling formed similar major groupings. The semi-automated fluorescence-based **AFLP** technique offered significant improvements on fragment sizing and data handling. It was also more accurate for **detection** and more efficient than the radioactive labelling method. This study shows that the **AFLP** technique is a reliable tool for differentiating bermudagrass genotypes and for determining genetic relationships among them.

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Divergent and Reticulate Species Relationships in Leucaena (Fabaceae) Inferred from Multiple Data Sources: Insights into Polyploid Origins and nrDNA Polymorphism .
Hughes, Colin E
Bailey, C. Donovan; Harris, Stephen A
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ABSTRACT: Previous analyses of species relationships and polyploid origins in the mimosoid legume genus Leucaena have used chloroplast **DNA** (cpDNA) restriction site data and morphology. Here we present an analysis of a new

DNA sequence data set for the nuclear ribosomal **DNA** (nrDNA) 5.8S subunit and flanking ITS 1 and ITS 2 spacers, a simultaneous analysis of the morphology, ITS and cpDNA data sets for the diploid species, and a detailed comparison of the cpDNA and ITS gene trees, which include multiple accessions of all five tetraploid species. Significant new insights into species relationships and polyploid origins, including that of the economically important tropical forage tree L. leucocephala, are discussed. Heterogeneous ITS copy types, including 26 putative pseudogene sequences, were found within individuals of four of the five tetraploid and one diploid species. Potential pseudogenes were **identified** using two pairwise comparison approaches as well as a tree-based method that compares observed and expected proportions of total ITS variation contributed by the 5.8S subunit optimized onto branches of one of the ITS gene trees. Inclusion of putative pseudogene sequences in the analysis provided evidence that some pseudogenes in allopolyploid L. leucocephala are not the result of post-allopolyploidization gene silencing, but were inherited from its putative diploid maternal progenitor L. pulverulenta. Reprinted by permission of the publisher.